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Title:
Perfect score:
Sequence:
                                                                                                                                                                                   Database :
                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                         PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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2427
1 EVQLQQSGPELVKPGASVMI.....RHEGLKNYYLKKTISRSPGK 454
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## ·SUMMARIES

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	1028	1049	1054.5	1058	1059	1072.5	1072.5	1080.5	1080.5	1087	1100	1112	1145	1150	1159	1170	1202.5	1286.5	_		1385.5	1414	1419	1439	1797	1832.5	1835	2135	2190.5	Score
	42.4	43.2	43.4		•	44.2	44.2	44.5	44.5	44.8	45.3	45.8	47.2		47.8	48.2	49.5	53.0	54.4	54.7	57.1	58.3	8			75.5		88.0	90.3	Query Match L
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	Ig gamma 3 c	Ig gamma 2b chair	Ig gamma-4 c	Ig gamma 2a	gamma-2 chain	Ig gamma-3	Ig gamma-3 chain	gamma-2 chain	gamma chain C	gamma-	Ig gamma-2a	Ig gamma-1 chain	gamma-1 chain	gamma-1	gamma-3 chain	Ig gamma	Ig	Ig heavy	· Ig gamma-1 c	Ig gamma-2b	Ig gamma-2a	Ig gamma-2a		mon	Ig gamma-2b	Ig gamma-2a	Ig gamma-2a	Ig gamma-2b cha	Ig gamma-2b cha	Description

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31.8	31.9	31.9	32.1	32.1	32.2	33.7	33.7	35.2	36.4	37.8	40.7	41.6	41.8	42.1	4.4
289	234	213	214	221	255	627	549	231	277	374	327	548	246	328	000
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G3HUWI	PT0207	S68213	PC4202	S49220	S31866	S14683	S04845	PC4155	147162	869339	806611	S38864	S38950	I47158	(((())
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## ALIGNMENTS

O)	A; Accession: A26233 A; Accession: A26233 A; Molecule type: DNA A; Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 < OL	Nature 296, 761-763, 1982  A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and g A;Reference number: A26233; MUID:82173203  A:Contents: h allele	A;ACCESSION: A20234 A;Molecule type: DNA A;Residues: 138-172,'p',174-189,'FP',193-376,'T',378-474 <tu2> R;Ollo, R.; Rougeon, F.</tu2>	A; Reference number: A26232; MUID:80081502	A, Molecule type: mRNA A; Residues: 138-172,'p',174-189,'FP',193-376,'T',378-474 <tu1> A; Residues: 138-172,'p',174-189,'FP',193-376,'T',378-474 <tu1> A; Note: Lys-474 is probably removed posttranslationally R; Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.</tu1></tu1>	A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b A;Reference number: A26235; MUID:80081501 A;Contents: MPC 11 A;Accession: A26235	A; Cross references: GB.300461 A; Oross references: GB.300461 A; Note: the sequence was determined from the germline gene R; Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R. Science 206. 1299-1303. 1979	_	349.1; PID:g54827	RESULT 1  G2MS11  Ig gamma-2b chain - mouse  C; Species: Mus musculus (house mouse)  C; Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000  C; Accession: S25057; A02157; A026335; A26232; A36233; A53598  R; Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. submitted to the EMBL Data Library, July 1992  A; Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi A; Reference number: S25057

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A;Introns: 138/1; 236/1; 258/1; 368/1
A;Introns: 138/1; 236/1; 258/1; 368/1
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin c region; immunoglobulin homology (Superfamily: immunoglobulin c region; immunoglobulin homology (Superfamily: heterotetramer; immunoglobulin pistale-22/Domain: immunoglobulin homology (Superfamily: heterotetramer; immunoglobulin pistale-236/ZPCPC (Superfamily: heterotetramer); immunoglobulin homology (Superfamily: heterotetramer); immunoglobulin 
                                                                                                                                       Ig gamma-2b chain precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence_revision 30-Sep C;Accession: S01321 R;de Waele, P.; Feys, V.; van de Voorde, A.; Eur. J. Biochem. 176, 287-295, 1988
                                                                                                                                                                                                                                                                                                                              RESULT
S01321
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A;Accession: A53598
A;Status: preliminary
A;Molecule type: protein
A;Residues: 234-251 <KIM>C;Comment: The a allele sequence is shown.
A; Molecule type: mRNA
A; Residues: 1-475 < DE
                                                       A; Title: Expression in non-lymphoid cells of A; Reference number: S01320; MUID:88329081 A; Accession: S01321
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Pred. No. 1.4e-123;
Pred. No. 1.4e-123;
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                                                                                                            mouse recombinant immunoglobulin
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A; Molecule type: mRNA
A; Residues: 1-469 <DUC>
A; Residues: 1-469 <DUC>
A; Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
A; Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 276-345/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision
C:Accession: S37483
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                                                                                   Query Match
Best Local :
                                                                     Matches
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QIQLQQSGPELVKPGASVKISCKASGYTFTDYYINWVKQKPGQGLKWIGWIYPASGNTKY
                    EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSIF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 418
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                                                                   al Similarity
345; Conser
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                                                                                   Score 1835;
Pred. No. 2.
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Pred. No. 3e-120;
                                                                                                                                                                                                                                                                                                                   February
                                                                   Mismatches
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                                                                                 ; DB 2;
2.2e-102;
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C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
C:Accession: S40295
R:Klebert, S: Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 ac
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V
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F;1-117/Domain: V-D-J region <CHD>
F;118-446/Domain: C region <CHP>
F;118-214/Domain: C1 region <CHI>
F;118-214/Domain: C1 region <CHI>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;341-446/Domain: C3 region <CH3>
F;341-446/Domain: C3 region <CH3>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: C3 region <CH3>
F;360-427/Domain: munoglobulin homology <MM>
F;360-427/Domain: munoglobulin homology <
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A; Accession: $40295
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ;1/Modified site: pyrrolidone carboxylic acid (Gln) *status experimental;22-96,144-199,261-321,367-425/Disulfide bonds: *status predicted;132/Disulfide bonds: interchain (to light chain) *status predicted;132/Disulfide bonds: interchain *status predicted;224,227,229/Disulfide bonds: interchain *status predicted
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                 SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAGAYYFDYWGQGTTLTVSSAK 120
                                                                                                                                                              VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
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NEKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCA-RGGKFAMDYWGQGTSVTVSSAK
                                                                                                                               QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKY
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                                                                                                                                                                                                                                                                                                                                                                                                                       carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                       75.5%;
                                                                                                                                                                                                                                                                                   Score 1832.5; DE Pred. No. 3e-102;
                                                                                                                                                                                                                                                            Mismatches
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#status experimental
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin c region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunog C;Keywords: immunoglobulin homology cIMM> F;143-212/Domain: immunoglobulin homology cIMM> F;352-369/Domain: intracellular #status predicted <TMM> F;352-369/Domain: intracellular #status predicted <TMM> F;186/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                   A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-335, K; <xX2> A;Residues: 1-335, K; <xX2> C;Comment: The sequence of residues 1-334 was assumed to be identical with the corres C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The hat it contains an alternative 3' end, encoded in separate exons, that is homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 335-378 <ROG>
A; Residues: 335-378 <ROG>
A; Note: the translation of the first exon of the membrane-bound segment
A; Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:J00462
R;Rogers, J.; Choi, E.; Souza,
Cell 26, 19-27, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T. Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982 A;Title: Nucleotide sequences of gene segments encoding A;Reference number: A02154; MUID:822222190 A;Accession: C02154
                                                                                                                                                                                                                      A; Introns: 1/1; 98/1; 120/1; 230/1; 335/1; 378/3
                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Gene segments encoding transmembrane A; Reference number: A02158; MUID:82115295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig gamma-2b chain C region, membrane-bound form - mouse C;Species: Mus musculus (house mouse) C;Decte: 17-Dec-1982 #sequence_revision 31-Mar-1991 #text_change C;Accession: C02154; A02158; B02157
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A; Accession: B02157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Complete nucleotide sequence of immunoglobulin A; Reference number: A02157; MUID:80120716
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A; Residues: 335-405 < YAM>
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A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a A;Reference number: JC5810; MUID:98063277

A;Accession: PC4436
A;Molecule type: protein
A;Residues: 1-444 <AKA>
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                                                                                                                                                                                                                                                                                                                      61 K-YAESVRGRFTISRDDSKSSVYLQMNRLREEDTATYYCCRTPWVYAMDCWGQGTSVIVS
                                                                                                                                                                                                                                                                                                                                                                58
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                                       THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI 357
                                                                                                  APNLEGGPSVFIFPDNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ
                                                                                                                                                                                 GLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCP 237
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  PREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYT
                                                                                                                                                                                                                                                               SAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQS 177
                                                                                                                                                                                                                                                                                                                                                                                                   EVQXVETGGGLVRPGNSLKLSCLTSGFTFSNYRMHWLRQPPGKRLEWIAVITVKSDNYGA 60
                                                                            VPEVS - - - SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQ
                                                                                                                                                            DLYTLSSSYTVPSSTWPSETVTCNVAHPASSTKVDKKIVP-----RDC-GCKPC-ICT
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                                                                                                                                                                                                                                                                                                                                               SIFSPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRAGAYYFDYWGQGTTLTVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                          EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGI---NPYYGG 57
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8; Mismatches 102;
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A;Cross-references: GB:V00798; NID:g51835; PIDN:CAA24178.1; PID:g1333984
R;Yamawaki-Kataoka, Y; Miyata, T; Honjo, T.

Nucleic Acids Res. 9, 1365-1381, 1981
A;Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and A;Reference number: A32657; MUID:81198976
A;Accession: A32657
A;Molecule type: DNA
A;Residues: 1-330 <YAM>
A;Cross-references: GB:J00470
A;Note: the sequence was determined from the germline gene
R;Ollo, R.; Auffray, C.; Moschamps, C.; Rougeon, F.
Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2446, 1981
A;Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggest
A;Reference number: A32658; MUID:8123894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Determination of the primary structure of a mouse Igo
A;Reference number: A32659; MUID:74175517
A;Contents: annotation; myeloma protein MOPC 173
A;Note: this is one paper in a series reporting the sequence;
A;Note: this sequence differs from that shown at a number of p
R;de Preval, C; Fougereau, M.
Eur. J. Biochem. 30, 452-462, 1972
A;Title: Determination of the primary structure of a mouse gam
A;Reference number: A32660; MUID:73056887
A;Gontents: annotation; MOPC 173, disulfide bonds
C;Genetics: 171,0847, 11471, 22471
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;15/Disulfide bonds: interchain (to light chain) #status experimental
F;27-82,144-204,250-308/Disulfide bonds: #status experimental
F;107,110,112/Disulfide bonds: interchain (to heavy chain) #status exp
F;180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                               hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Reywords: alternative splicing; duplication; glycoprotein; heterotetramer; immu F;20-84/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                F;20-84/Domain: immunoglobulin F;98-113/Region: hinge
                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 1/1; 98/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A32658
A;Molecule type: DNA
A;Residues: 1-330 <OLL>
A;Note: the sequence was determined from the germline
A;Note: Lys-330 is removed posttranslationally
A;Note: Lys-330 is removed posttranslationally
R;Bourgois, A.; Fougereau, M.; Rocca-Serra, J.
Eur. J. Blochem. 43, 423-435, 1974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig gamma-2a chain C region, secreted for Species: Mus musculus (house mouse) C;Date: 30-Sep-1980 #sequence_revision C;Accession: A02152; A32657; A32658
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A; Residues: 1-330 <SIK>
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                                              experimental
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Conservative

30;

Score 1419; D Pred. No. 9.4e 00; Mismatches

DB 1; .4e-78; 36;

Length 330;

Indels

6,

Gaps

2

58.5%; 78.6%;

78.5%;

2.3e-77;

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A;Introns: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associ C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; F;137-206/Domain: immunoglobulin homology C!MM>
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G2MSAM
                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 373-399 <RES>
A;Residues: 373-399 <RES>
A;Cross-references: GB:M35032; NID:g194478; PIDN:AAA37919.1; PID:g387217
C;Comment: The sequence of residues 1-328 was assumed to be identical with the correspon C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The maint it contains an alternative 3' end, encoded in separate exons, that is homologous with
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Sequence and polyadenylation site determination A; Reference number: 157809; MUID:90097953 A; Accession: 157809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-329, Kr (YA2>
R; Hall, B.; Milcarek, C.
MOl. Immunol. 26, 819-826, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 329-399 YAM>
A; Cross references: GB:J00471
A; Cross references: GB:J00471
A; Note: the sequence was determined from the R; Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T. Nucleic Acids Res. 9, 1365-1381, 1981
A; Title: The complete nucleotide sequence of A; Reference number: A32657; MUID:81198976
A; Accession: B32657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
A;Title: Nucleotide sequences of gene segments encodia A;Reference number: A02154; MUID:82222190
                                                                                                                                                                                                                                     C; Genetics:
A; Introns: 1/1; 98/1; 114/1;
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                                                                                    ;346-363/Domain:
;364-399/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g gamma-2a chain C region, membrane-bound form - mouse
;Species: Mus musculus (house mouse)
;Date: 19-Feb-1984 #sequence_revision 31-Mar-1991 #text_change
;Accession: A02154; B32657; I57809
  Query
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VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
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                                                                  site:
                                                              transmembrane #status predicted intracellular #status predicted e: carbohydrate (Asn) (covalent)
    30
  Score
  1414;
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Length 399;
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Matches

Local Si hes 259;

Similarity

Conservative

1;

Gaps

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119

AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 178

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A; McCeule type: mRNA
A; Residues: 1-335 <SCH>
A; Rolecule type: mRNA
A; Residues: 1-335 <SCH>
A; Cross-references: GB:J00479
A; Experimental source: strain C57BL/6
R; Dognin, M.J.; Lauwereys, M.; Strosberg, A.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981
A; Title: Multiple amino acid substitutions between murine gamma 2a heavy chain Fc reg
A; Reference number: A32656; MUID:82037777
A; Accession: A32656
A; Molecule type: protein
A; Residues: 118-267, 'E', 269-328, 'G', 330-334 <DOG>
C; Comment: Tys-335 is removed posttranslationally.
C; Comment: The sequence differs from that of the a allele, from BALB/c mice, at 15% o
C; Comment: The sequence differs from that of the subunit consists of two identical light (
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl
F; 20-84, Domain: immunoglobulin homology <IM1>
F; 98-118/Region: hinge
F; 148-211/Domain: immunoglobulin homology <IM2>
F; 124-211/Domain: immunoglobulin homology <IM2>
F; 128-31, 149-209, 255-313/Disulfide bonds: #status predicted
F; 27-82, 149-209, 255-313/Disulfide bonds: #status predicted
F; 108, 117/Disulfide bonds: interchain (to heavy chain) #status predicted
F; 108, 119-09, 255-313/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: A02153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig gamma-2a chain C region, secreted form (allele b) - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change C;Accession: A02153; A32656
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Pred. No. 9.5e-7
3; Mismatches
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A;Title: Evolution of the rat immunoglobulin gamma he A;Reference number: PS0017; MUID:89232738
A;Reference number: PS0017; MUID:89232738
A;Recession: PS0018
A;Molecule type: DNA
A;Residues: 1-333 < GRU>
R;Brueggemann, M; Free, J; Diamond, A.; Howard, J;
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A;Ritle: Immunoglobulin heavy chain locus of the rat:
A;Reference number: A25941; MUID:86287397
A;Accession: B35941
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 227-333 < GRZ>
C;Genetics:
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C;Superfamily: immunoglobulin C region;
C;Keywords: immunoglobulin
F;20-82/Domain: immunoglobulin homology
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pS0018
rg gamma-2b chain C region - rat
Ig gamma-2b chain C region - rat
C;Speciles: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999
C;Accession: PS0018; B25941
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Gene 74, 473-482, 1988
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C; Species: Ovis orientalis aries, Ovis am
C;Date: 13-Jan-1995 #sequence_revision 13
C;Accession: S31459
R;Patri, S; Nau, F.
submitted to the EMBL Data Library, Decem
A;Reference number: S31459
A;Reference s31459
A;Accession: S31459
A;Accession: S31459
A;Accession: RNA
A;Residues: 1-472 < PATD
A;Control of the control of the con
                                                              Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine N;Alternate names: Ig gamma-1 chain C region (clone 8.10) C;Species: Bos primigenius taurus (cattle) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_C;Accession: $22080; $06610; A31303 R;Sanders, P.G.
    A; Reference number: A; Accession: S22080
                      submitted to the EMBL Data Library, A; Reference number: S22080
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C;Superfamily: immunoglobulin C region; immunog
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                          SYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                             APQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNG--HTEENYKDTAPVLDSDG 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVRLQESGPSLATLLQTLSVTCTISGFSLNNYGVDWVRQAPGKALEWLGG-SGYDEDIDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTARTKPREEQFNSTFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRTISRTKGQAR
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Pred. No. 9.36
                                              November 1991
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351

307 291

367

248 231 196 76 60

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A; Molecule type: DNA
A; Residues: 142-470 < SYM>
A; Residues: 142-470 < SYM>
A; Cross-references: EMBL:X16701
A; Note: the sequence was determined from the germline gene
C; Genetics:
A; Gene: 1g CH gamma-1
A; Introns: 98/1; 111/1; 221/1
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: 91/copyrotein; heterotetramer; immunoglobulin; membrane protein
F; 161-225/Domain: immunoglobulin homology < IMM>
F; 318/Binding site: carbohydrate (Asn) (covalent) #status predicted
A;Reference number: S00847; MUID: A;Accession: S00847
A;Accession: S00847
A;Molecule type: mRNA
A;Residues: 1-329 <BRU>
A;Cross-references: EMBL:X07189;
                                                                       Ig gamma-2c chain C region - rat (fragment)
(; Species: Rattus norvegicus (Norway rat)
C; Date: 01-Dec-1989 #sequence_revision 01-Dec-1989
C; Accession: $00847
R; Brueggemann, M.; Delnastro-Galfre, P.; Waldmann,
Eur. J. Immunol. 18, 317-319, 1988
A; Title: Sequence of a rat immunoglobulin gamma-2c
A; Reference number: $00847; MUID: 88166903
                                                                                                                                                                                                                               RESULT
S00847
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A; Molecule
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A;Title: Structure of bovine immunoglobulin A;Reference number: 506610, MUID:90097956
A;Accession: S06610
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A; Cross-rof-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPAL 174
                                                                                                                                                                                                                                                                                                                          FIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
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                                                                                                                                                                                                                                                                                                        FLYSKLRVDRNSWQEGDTYTCVVMHEALHNHYTQKSTSKSAGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRA-----GAYYFDYWGQGTTL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQLRESGPSLVKPSQTLSLTCTVSGFSLSSYALTWVRQAPGKALEWVGGITS-GGTTYY 78
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54.2%;
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 NID:g57602; PIDN:CAA30169.1;
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Pred. No. 1.1e-69;
0; Mismatches 121;
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Ig gamma-3 chain C region, secreted form - mouse C;Species: Mus musculus (house mouse) c;Date: 17-Mar-1987 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999 C;Accession: B02156 R;Wels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker, EMBO, J. 3, 2041-2046, 1984
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                                                                                                                                                                                                                      F;136-205/Domain: immunoglobulin homology <IM2> F;242-309/Domain: immunoglobulin homology <IM3> F;179,322/Binding site: carbohydrate (Asn) (cov
                                                                                                                                                                                                                                                                                        A;Introns: 97/1; 113/1; 223/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology <IMI>
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A; Residues: 1-329 <WEL>
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Best Local Similarity
Matches 229; Conserv
                                                                                                                                  Matches
                                                                                                                                                                     Query Match
                                181
                                                                                   121 TTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLY 180
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                                                                                                                                                         Local
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                 TMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPAPN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 178
SLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR----IPKPSTPPGSSCPPGN
                                                                  TTAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQSGFY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDTDSWMRGDIYTCSVVHEALHNHHTQKNLSRSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARTTAPSVYPLVPGCSGTSGSLVTLGCLVKGYFPEPVTVKWNSGALSSGVHTFPAVLQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPPREQMSKNKVSLTCMVTSFYPASISVEWERNGELEQDYKNTLPVLDSDESYFLYSKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYTLSSSVTVPSSTWSSQTVTCSVAHPATKSNLIKRIEPRRP----KPRPPTDIC-SCD- 114
                                                                                                                                                       Similarity
                                                                                                                                     Conservative
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                                                                                                                                                     48.2%;
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Pred.
                                                                                                                                                       Score 1170;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                 from
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                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1202.5;
No. 7.6
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                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IgG3
                                                                                                                                                                                                                         (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                               germline
                                                                                                                                     DB 1;
5.6e-63;
ies 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .6e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constant region
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                                                                                                                                                                     Length
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                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P.W.;
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunog F;19-83/Domain: immunoglobulin homology <IM1>
F;97-112/Region: hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: the sequence was determined from the germline gene R;Komaromy, M.; Clayton, L.; Rogers, J.; Robertson, S.; Kettman, J.; Wall, Nucleic Acids Res. 11, 6775-6785, 1983
A;Title: The structure of the mouse immunoglobulin in gamma-3 membrane general R;Reference number: A02155; MUID:84041483
A;Accession: A02155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig gamma-3 chain C region, membrane-bound form - mouse C;Species: Mus musculus (house mouse) C;Species: Aug-1986 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999 C;Accession: A02156; A02155
R;Wels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker EMBO J. 3, 2041-2046, 1984
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                                                                                                                                                                                                                                                              Ϋ́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;136-205/Domain: immunoglobulin homology <IM2>
F;242-709/Domain: immunoglobulin homology <IM3>
F;244-362/Domain: transmembrane #status predicted <TMM>
F;363-398/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 328-332,'G',334-341,'Q',343-387,'F',389-398 <KOM>
A;Residues: 328-332,'G',334-341,'Q',343-387,'F',389-398 <KOM>
A;Rose: the sequence was determined from the germline gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Structure analysis of the murine IgG3 constant region gene A;Reference number: A02156; MUID:85027161
A;Accession: A02156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:J00451; NID:g194392; PIDN:AAB59655.1; PID:g194433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       179,322/Binding site:
                        296
  116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 TSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 454
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                                                                                                                                    TMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPAPN 240
                                                                                                                                                                                                                                           TTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLY 180
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ILGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPRE 175
                                                                                                      SLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR-----IPKPSTPPGSSCPPGN 115
                                                                                                                                                                                                            TTAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQSGFY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDSWLQGEIFTCSVVHEALHNHHTQKNLSRSPGK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVD 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPP
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                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                            47.8%;
                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                              Score 1159; DB 1; Length 398; Pred. No. 3.7e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        duplication; glycoprotein; heterotetramer; immunoglob
                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                     361 PAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNMK 420
TSKWEKTDSFSCNVRHEGLKNYYLKKTISRSP 452
| | : : |:|:| || |:::: : :|:|||
TDSWLQGEIFTCSVVHEALHNHHTQKNLSRSP 327
                                                                                                                                                          EDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILPP
                                                                                                                                          AQYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPP
                                                                     PREQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVD
                                                                                                                                                                            360
                                                                                                                                          235
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Search completed: June 18, 2001, 15:32:45 Job time: 163 sec

